

1-2 rni

Patent

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:48:30 ; Search time 78.5 Seconds  
(without alignments)  
286.029 Million cell updates/sec

Title: US-10-777-592-1  
Perfect score: 12  
Sequence: 1 gttacagcacag 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
c	1	12	100.0	18	3	US-09-167-109-161
	2	12	100.0	351	3	US-09-513-999C-18778
	3	12	100.0	443	3	US-09-397-787-194
	4	12	100.0	485	3	US-09-621-976-3704
	5	12	100.0	503	3	US-09-621-976-3703
	6	12	100.0	601	3	US-09-949-016-58228
	7	12	100.0	601	3	US-09-949-016-58229
						Sequence 161, App
						Sequence 18778, A
						Sequence 194, App
						Sequence 3704, Ap
						Sequence 3703, Ap
						Sequence 58228, A
						Sequence 58229, A

6-3 rnpbm

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:12 ; Search time 502 Seconds  
(without alignments)  
293.728 Million cell updates/sec

Title: US-10-777-592-1  
Perfect score: 12  
Sequence: 1 gttacagcacag 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	12	100.0	18	6 US-10-067-125-161	Sequence 161, App

1-4  
rnpba

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:45 ; Search time 95.25 Seconds  
(without alignments)  
201.394 Million cell updates/sec

Title: US-10-777-592-1  
Perfect score: 12  
Sequence: 1 gttacagcacag 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	12	100.0	12	6	US-10-777-592-1
2	12	100.0	25	9	US-11-348-413-602062
3	12	100.0	25	9	US-11-348-413-602063
4	12	100.0	25	9	US-11-348-413-602064
5	12	100.0	25	9	US-11-348-413-602065
6	12	100.0	25	9	US-11-348-413-602066
7	12	100.0	25	9	US-11-348-413-602067

1-5 rst

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:43:03 ; Search time 1366.75 Seconds  
(without alignments)  
490.969 Million cell updates/sec

Title: US-10-777-592-1  
Perfect score: 12  
Sequence: 1 gttacagcacag 12

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
c	1	12	100.0	101	5	CF091895	CF091895 QHM9L17.y
	2	12	100.0	101	10	DR698128	DR698128 An_1669.C
	3	12	100.0	106	9	DR071094	DR071094 RTDK1_17_

3-1 rrg  
PCR prim

OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:35:34 ; Search time 262.042 Seconds  
(without alignments)  
505.541 Million cell updates/sec

Title: US-10-777-592-3  
Perfect score: 19  
Sequence: 1 ctagttctgcatctgctca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
<hr/>							
c	1	19	100.0	19	12	ADO22998	Ado22998 Human amy
	2	19	100.0	24	4	AAD18303	Aad18303 Human pre

3-2 rni

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:48:30 ; Search time 124.292 Seconds  
(without alignments)  
286.029 Million cell updates/sec

Title: US-10-777-592-3  
Perfect score: 19  
Sequence: 1 ctagttctgcatctgctca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	19	100.0	33	3	US-09-481-980A-4	Sequence 4, Appli
c 2	19	100.0	300	3	US-09-964-899-3	Sequence 3, Appli
c 3	19	100.0	300	3	US-09-964-899-4	Sequence 4, Appli
c 4	19	100.0	303	3	US-09-422-569-1	Sequence 1, Appli
c 5	19	100.0	315	3	US-09-823-153-3	Sequence 3, Appli
c 6	19	100.0	354	2	US-08-729-345-2	Sequence 2, Appli
c 7	19	100.0	354	3	US-09-422-569-3	Sequence 3, Appli

3-3 m p b m

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:12 ; Search time 794.833 Seconds  
(without alignments)  
293.728 Million cell updates/sec

Title: US-10-777-592-3  
Perfect score: 19  
Sequence: 1 ctagttctgcatctgtca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	19	100.0	24	6 US-10-234-961-14	Sequence 14, Appl

3-4  
rnpbA

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:45 ; Search time 150.812 Seconds  
(without alignments)  
201.394 Million cell updates/sec

Title: US-10-777-592-3  
Perfect score: 19  
Sequence: 1 ctagtctctgcatctgctca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match					
1	19	100.0		19	6	US-10-777-592-3	Sequence 3, Appli
2	19	100.0		38	6	US-10-515-919A-25	Sequence 25, Appl
c 3	19	100.0		465	9	US-11-327-124A-48	Sequence 48, Appl
c 4	19	100.0		977	8	US-11-266-748A-191697	Sequence 191697,
c 5	19	100.0		977	8	US-11-266-748A-225960	Sequence 225960,
6	19	100.0		1645	8	US-11-266-748A-162725	Sequence 162725,
c 7	19	100.0		1779	8	US-11-266-748A-22074	Sequence 22074, A



3-5 st

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:43:03 ; Search time 2164.02 Seconds  
(without alignments)  
490.969 Million cell updates/sec

Title: US-10-777-592-3  
Perfect score: 19  
Sequence: 1 ctagttctgcacatctgctca 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est3:\*
- 3: gb\_est4:\*
- 4: gb\_est5:\*
- 5: gb\_est6:\*
- 6: gb\_htc:\*
- 7: gb\_est2:\*
- 8: gb\_est7:\*
- 9: gb\_est8:\*
- 10: gb\_est9:\*
- 11: gb\_gss1:\*
- 12: gb\_gss2:\*
- 13: gb\_gss3:\*
- 14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	% Match	Query Length	DB	ID	Description
c	1	19	100.0	136	2	BF997090	BF997090 QV3-GN020
	2	19	100.0	140	7	AW845176	AW845176 QV0-CT001
	3	19	100.0	180	1	AI905870	AI905870 IL-BT101-

PCR Run

2-1  
rng

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:35:34 ; Search time 234.458 Seconds  
(without alignments)  
505.541 Million cell updates/sec

Title: US-10-777-592-2  
Perfect score: 17  
Sequence: 1 atgctgccccggtttggc 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : N\_Geneseq\_8:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*
- 15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	17	100.0	19	14	ADV92881	
c	2	17	100.0	19	14	ADV93080	Adv92881 Amyloid p Adv93080 Amyloid p

2-2 mi

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:48:30 ; Search time 111.208 Seconds  
(without alignments)  
286.029 Million cell updates/sec

Title: US-10-777-592-2  
Perfect score: 17  
Sequence: 1 atgctgcccgggtttggc 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents\_NA:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					Description
Result	Query	Score	Match	Length	DB	ID	
No.							
c	1	17	100.0	20	2	US-08-331-389A-1	Sequence 1, Appli
c	2	17	100.0	20	3	US-09-192-657A-1	Sequence 1, Appli
	3	17	100.0	25	3	US-08-339-708A-15	Sequence 15, Appl
	4	17	100.0	29	7	PCT-US94-04026-5	Sequence 5, Appli
	5	17	100.0	31	2	US-08-664-872-6	Sequence 6, Appli
	6	17	100.0	31	3	US-09-019-973-6	Sequence 6, Appli
	7	17	100.0	31	3	US-09-260-897-6	Sequence 6, Appli

2-3  
rnpbm

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:12 ; Search time 711.167 Seconds  
(without alignments)  
293.728 Million cell updates/sec

Title: US-10-777-592-2  
Perfect score: 17  
Sequence: 1 atgctgccccggtttggc 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_Main:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 11: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 12: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*
- 13: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*
- 14: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11B\_PUBCOMB.seq:\*
- 15: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11C\_PUBCOMB.seq:\*
- 16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	17	100.0	19	10	US-10-877-889-9	Sequence 9, Appli

2-4 rnpbn

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:52:45 ; Search time 134.938 Seconds  
(without alignments)  
201.394 Million cell updates/sec

Title: US-10-777-592-2  
Perfect score: 17  
Sequence: 1 atgctgccccggtttggc 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2226170 seqs, 799283156 residues

Total number of hits satisfying chosen parameters: 4452340

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Published\_Applications\_NA\_New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq1:\*
- 9: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11\_NEW\_PUB.seq2:\*
- 10: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query Match	Length			
1	17	100.0	17	6	US-10-777-592-2	Sequence 2, Appli
2	17	100.0	1199	8	US-11-266-748A-184215	Sequence 184215,
3	17	100.0	1199	8	US-11-266-748A-191695	Sequence 191695,
4	17	100.0	1319	8	US-11-266-748A-59195	Sequence 59195, A
5	17	100.0	1629	8	US-11-266-748A-184214	Sequence 184214,
6	17	100.0	3416	8	US-11-269-857-1	Sequence 1, Appli
7	17	100.0	301692	8	US-11-266-748A-28776	Sequence 28776, A

2-5 1st

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2006, 21:43:03 ; Search time 1936.23 Seconds  
(without alignments)  
490.969 Million cell updates/sec

Title: US-10-777-592-2  
Perfect score: 17  
Sequence: 1 atgctgccccggtttggc 17

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est3:\*  
3: gb\_est4:\*  
4: gb\_est5:\*  
5: gb\_est6:\*  
6: gb\_hlc:\*  
7: gb\_est2:\*  
8: gb\_est7:\*  
9: gb\_est8:\*  
10: gb\_est9:\*  
11: gb\_gss1:\*  
12: gb\_gss2:\*  
13: gb\_gss3:\*  
14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	17	100.0	154	1	AU077057	AU077057 AU077057	
2	17	100.0	160	8	CN393892	CN393892 170005322	
3	17	100.0	217	9	DA188413	DA188413 DA188413	